SEQUENCE LISTING

	<110			LI-		нs.											
	<120)> s	iRNA	BAS	ED M	ETHO	DS F	OR T	REAT	ING	ALZH	EIME	R'S 1	DISE	ASE		
	<130)> H	MV-0	90.0	1												
				7,53 08-0													
			•	S04/ 08-0		3											
				3,61 08-0													
	<160> 20																
	<170> PatentIn Ver. 3.2																
	<210 <211 <212 <213	.> 1! !> D!	AV	sapi	ens												
<220> <221> CDS <222> (1)(1506)																	
	<400			~~~	at ~		t ~~	ata	ata	a+~	+~~	2 t a	~~~	~~~	gg 2	ata	48
											tgg Trp						40
							_				cgg Arg	_					96
	ggc Gly	ctg Leu	999 Gly 35	ggc Gly	gcc Ala	ccc Pro	ctg Leu	999 Gly 40	ctg Leu	cgg Arg	ctg Leu	ccc Pro	cgg Arg 45	gag Glu	acc Thr	gac Asp	144
								Arg		Gly	agc Ser						192
											tac Tyr 75						240
			_		_	_	_				ctg Leu		-				288
											ccc Pro						336

	_	 _	_		agc Ser				_			-		384
				_	ggc Gly 135						-			432
					ggc Gly									480
					gac Asp									528
					gcc Ala									576
	_				gac Asp		_	_	_	-				624
					ctt Leu 215									672
	_	 _	_		gtc Val			_	_					720
					ggc Gly									768
					atc Ile				_					816
_	_	_	_	_	aag Lys					_	_	_		864
					ctt Leu 295									912
-	_			_	gca Ala	_			_		_		_	960
					cag Gln									1008
					gtc Val						_			1056

acc aac cag Thr Asn Gln 355	_			_								
cca gtg gaa Pro Val Glu . 370												
atc tca cag Ile Ser Gln : 385	_	Gly Thr V										
ggc ttc tac q Gly Phe Tyr					-							
gtc agc gct t Val Ser Ala (His Asp G										
ggc cct ttt g Gly Pro Phe N 435	-											
cag aca gat o Gln Thr Asp (450			_	-								
atc tgc gcc o Ile Cys Ala I 465	_	_	_									
cgc tgc ctc c Arg Cys Leu A												
atc tcc ctg c Ile Ser Leu I 5					1506							
<210> 2 <211> 501 <212> PRT <213> Homo sapiens												
<400> 2 Met Ala Gln A 1	ala Leu Pro 5	Trp Leu L	Leu Leu Trp 10	Met Gly Ala	Gly Val 15							
Leu Pro Ala H	is Gly Thr 20		Sly Ile Arg 25	Leu Pro Leu 30	Arg Ser							
Gly Leu Gly G 35	Sly Ala Pro	Leu Gly L 40	eu Arg Leu	Pro Arg Glu 45	Thr Asp							
Glu Glu Pro G 50	du Glu Pro	Gly Arg A 55	arg Gly Ser	Phe Val Glu 60	Met Val							
Asp Asn Leu A 65	rg Gly Lys 70	Ser Gly G	in Gly Tyr 75	Tyr Val Glu	Met Thr 80							

- Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser 85 90 95
- Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr 100 105 110
- Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val 115 120 125
- Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp 130 135 140
- Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
- Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp 180 185 190
- Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro 195 200 205
- Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln 210 215 220
- Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile 225 230 235 240
- Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg 245 250 255
- Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln 260 265 270
- Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val 275 280 285
- Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala 290 295 300
- Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp 305 310 315 320
- Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr 325 330 335
- Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val 340 345 350
- Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg 355 360 365
- Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala 370 375 380
- Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu 385 390 395 400

Gly	Phe	Tyr	Val	Val 405	Phe	Asp	Arg	Ala	Arg 410	Lys	Arg	Ile	Gly	Phe 415	Ala	
Val	Ser	Ala	Cys 420	His	Val	His	Asp	Glu 425	Phe	Arg	Thr	Ala	Ala 430	Val	Glu	
Gly	Pro	Phe 435	Val	Thr	Leu	Asp	Met 440	Glu	Asp	Cys	Gly	Tyr 445	Asn	Ile	Pro	
Gln	Thr 450	Asp	Glu	Ser	Thr	Leu 455	Met	Thr	Ile	Ala	Tyr 460	Val	Met	Ala	Ala	
Ile 465	Cys	Ala	Leu	Phe	Met 470	Leu	Pro	Leu	Cys	Leu 475	Met	Val	Cys	Gln	Trp 480	
Arg	Cys	Leu	Arg	Cys 485	Leu	Arg	Gln	Gln	His 490	Asp	Asp	Phe	Ala	Asp 495	Asp	
Ile	Ser	Leu	Leu 500	Lys												
			1													
<212	L> 19 2> DN		sapie	ens												
<400> 3												19				
<210> 4 <211> 19 <212> DNA <213> Mus musculus																
<400> 4 gctttgtgga gatggtgga 1											19					
<210> 5 <211> 19 <212> DNA <213> Rattus sp.																
<400> 5 gctttgtgga gatggtgga																
<210> 6 <211> 19 <212> DNA <213> Mus musculus																
<400 actt		ıgc t	atgg	ıtgga	ı											19
<210 <211)> 7 .> 19)														

<212> <213>		sapiens
<400>		catggtaga
400000	egge	catggtaga
<210> <211>		
<212>	DNA	
<213>	Homo	sapiens
<400>	-	atcctggtg
33		
<210>		
<211> <212>		
<213>	Mus n	nusculus
<400>		
gacgct	caac	atcctggtg
<210>	10	
<211>	19	
<212> <213>		ıs sp.
<400>		-
		atcctggtg
<210>		
<211> <212>		
<213>	Mus m	nusculus
<400> gaaggt		attcttgtg
<210>		
<211> <212>		
		sapiens
<400>		
gaagct	acag	attctcgtt
~210×	1 2	
<210> <211>	19	
<212> .		sapiens
		£ 2222
<400> tggact		ggagtacaa

.

<210> 14	
<211> 19	
<212> DNA	
<213> Mus musculus	
<400> 14	
tggactgcaa ggagtacaa	19
<210> 15	
<211> 19	
<212> DNA	
<213> Rattus sp.	
<400> 15	
tggactgcaa ggagtacaa	1:
<210> 16	
<211> 19	
<212> DNA	
<213> Homo sapiens	
<400> 16	
ttggctttgc tgtcagcgc	1:
<210> 17	
<211> 19	
<212> DNA	
<213> Mus musculus	
<400> 17	
ttggctttgc tgtcagcgc	1:
<210> 18	
<211> 19	
<212> DNA	
<213> Rattus sp.	
·	
<400> 18	
ttggctttgc tgtcagcgc	1:
<210> 19	
<211> 19	
<212> DNA	
<213> Mus musculus	
400 10	
<400> 19	
tgggctttgc agtgagtcc	1
.210. 20	
<210> 20	
<211> 19	
<212> DNA	
<213> Homo sapiens	

<400> 20 tgggcttcgc agcgagccc

19